

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Zsebo et al.
- (ii) TITLE OF INVENTION: Stem Cell Factor
- (iii) NUMBER OF SEQUENCES: 104
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/635,249
 - (B) FILING DATE: 07-AUG-2000
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/486,546
 - (B) FILING DATE: 24-MAY-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/172,329
 - (B) FILING DATE: 21-DEC-1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/982,255
 - (B) FILING DATE: 25-NOV-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/684,535
 - (B) FILING DATE: 10-APR-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/589,701
 - (B) FILING DATE: 10-OCT-1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/573,616
 - (B) FILING DATE: 24-AUG-1990
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/537,198
 - (B) FILING DATE: 11-JUN-1990

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/422,383
- (B) FILING DATE: 16-OCT-1989

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Clough, David W.
- (B) REGISTRATION NUMBER: 36,107
- (C) REFERENCE/DOCKET NUMBER: 01017/35199

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 312/474-6300
- (B) TELEFAX: 312/474-0448
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr
1 5 10 15
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr
20 25 30
Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
35 40 45
Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser
50 55 60
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly
65 70 75 80
Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys
85 90 95
Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro
100 105 110
Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp
115 120 125
Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu
130 135 140
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu
145 150 155 160
Pro Pro Val Ala Ala
165

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /mod_base= Inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACRTTYTTNG GNGCRTTYTC YTCCAT

26

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 12 and 15
 - (D) OTHER INFORMATION: /mod_base= Inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AARAAATCYT CNGGNGTRAA RTT

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTATCNGGYT TYTT

14

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGARGARA AYGCCCCCAA RAA YGT

26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
CCNAAYGAYT AYATGWTMAC 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GGNGGNARCA TRAANGGYTT 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
ACCAKAARAT CTTYAAANCG ATC 23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
GTATTTTCAA TAGATCCATT GA 22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
CCAACTATGT CGCC 14

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTAGTCAAGC TGACTGATAA G 21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCAACAA TGACTAGGCA A 21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCAGAGTC AGTGTC 16

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAAGCTTG CCTTTCCTTA TGAAGAAGA 29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTTGTGA 38

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATAAATGCA AGTGATAATC C

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGTCGACC CGCGGAACCT TAAGTCCATG CAACAC

36

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG

36

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACCCGCGGT TAGGCTGCAA CAGGGGGTAA CATAAA

36

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTAATGTTG AAGAAACC

18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATGGTAGTA CAATTGTCAG AC 22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCTGACAAT TGTACTACCA TC 22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAATTTAGTG ACGTCTTTTA CA 22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGATGAGT TTTCTTTCAC GCAC 24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAATCATTCA AGAGCCCAGA ACCC 24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACATCCATC CCGGGGAC

18

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGCAATAT TTAAAGTCTC AAGAAGACC

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGCCGCGGC TCCTATAGGT GCTAATTGG

29

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCACCCT GTTGTGCTG GATCGCA

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTGTCTAGA CTTGTGTCTT CTTCATAAGG A

31

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCCCCCHGG

10

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT TTTTTTTTGG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTTTTTTTT TTTTTTTTAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTTTTTTTT TTTTTTTTCG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
TTCGGCCGAT CAGGCCCCC CCCC 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT 30

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
GGCCGGATAG GCCTCACNNN NNNT 24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
GGCCGGATAG GCCTCAC 17

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: join(660..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: join(720..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAAGTATCTT TCTATTGGCG AAGGACATGT TTTCCCATAA GTGGTAAACA AACTGTCTGC	60
ACATAATAAT TATCTTGCTG CCGTAAAGAT TAGGTTAAAT TCTGCCTTCG ATCTAAAAAC	120
ACACCCTTCT GTCAATCCGA GGAGCAGTGT GCTAGTCTAG AGGTCTAAAT GAAGGCTCCT	180
TTCACGGTTG TATTTCTGCT CCCCAAATTG TCCACATTTA AAAGGAGAGT GCTTCTTTTC	240
AGCCTTAGGC TCTGAATTTC ATGCATTCCCT CCATTTTCCG AGGTCCCCCC CAAGTGATAA	300
TTCTGTTACA CGTTGCTACA AGTTCATCCC TAATTGCCGT CAAGAACTG ACTGTAGAAG	360
GCTTACCACA GACGTTGTAA CCGACAGTAA AGCCATTGAA AGAGTAATTC AAACAGGATG	420
GAAGCCAGGA GTATTTTGTG GCTGTTGCTC TTTTCTTTT CAGTTTGGTG AGAGCAGCTT	480
GAATGCTTAA CATTTAAGCC ATCAGCTTAA AACAAAACAA AACAAAACAA AAAAAAACC	540
CGCTCTGGCA TATTTGCACT TAACACATAC GGTATAAGGT GTTACTGGTT TGCATAGTTC	600
TGGATTTTTT TTTTTTAAAA ACTGATGGAC ACCAAGAAAT GTTCTGTTC TTTGTTTAG	659
ACT TGG ATT ATC ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT	707
Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
CTC GTC AAA ACT CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA	755
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
1 5 10	
AAA GAC ATT ACA AAA CTG GTAAGTAAAG AATGATTTTG GCATCTATAA	803
Lys Asp Ile Thr Lys Leu	
15	
GTCTTCCCTG TGCTTGCTGA CCACATAGGT TCAGGGCACT CCCGACAGGA GTTCCCAGCT	863
TTCTAAGATA AGGAATCACT GTACGAGTCT GAAGTGCTTC TTCTGGGCAA ATGGGAGATG	923
CTTAGGTCAT GGAGGGTTTA TCTGTATAAC TGGCCCTTTG CACACCAACA AAGTGACTION	983
CTGGCTTTTG CCTGTTACCT ACTGTCTCCA GTCCTGGGCA TGGTATATAC TTAGGCACCC	1043
AAGATTGGAT TTACAACTCA AGCATTATAT ATTGGACAAC ACGGGGTATG AGATATTAAT	1103
GATATGTCAG GTTGGATGGA TGAGTTTTCT CAAGAAATTC TCTTGATTTT ACTCACGTTT	1163
TCATTTCTTG GTCTCTGTAG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA	1213
Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
20 25	
ACC CTC AAC TAT GTC GCC GGG ATG GAT GTT TTG GTATGTAGTC CACACACTTC	1266
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
30 35	
TGAGTTGCCT TTTAGTAGCT AATGGGTGAC CTGTGCTTAT TCACATTGAA GACATTATTT	1326
GCTCTTTGTC GTTTTTAGAT GTTGACCTAT AATTTTCCCT TCAAGCTGCT GCTAAGATTA	1386
TCAGTGAGCA TTTCAGTATG TGTTTTAAGC CTACTIONTAA AAAGGAAATG GCTCATCTTA	1446
GACGTAGCAA CCGATGTAA TTTTTCCCCA GGCATCTCTC AGAGGGACTT GAATGTAAAA	1506
ATCATGTAA ATTTCCCTCT TGGCTATGTT ATTTCTCATG GCTATGTTAT TCCTATTCGT	1566
ATTTCAATTA AAGGGACGGA ATATTTATTG TATTTCTGAA CTTTTTCAGG CATGCATCCG	1626
GGTCTTTGAA TAAAACACTA AGACTCCTTC TAGTAATGTT TGTAATCCTG TCTGTATCGA	1686

ATGTCTTTGA AAACGCAGTG ACTAAGCCAT AAATAATCTT CCACAGAACG TCCAGTGGTT	1746
CATGAACTTT GTATGTGGGG GTGGGGCAAG AATTGTCTCA CTATTGGTCA AGGAAGAGAA	1806
GGTAAGGTAT GCAAGGGTGG TTTAATCTTC TTCCGTGGAA GGACAAAATC ATCTATCATT	1866
TCCTCTGATC TCTATGCATT TGTTTGT TTTT GAACTGAATC TGA CTGAGC AAGAGTTGGC	1926
GTCCTGTGTT CTGAGGAAAC TCTTTGTCCT GCAGTCAGTG ACTAAAAGTG CTGAGAGATC	1986
TGAAGAGCAC TCTGAATCTG CCATATTTTT AATAGATGCT TTGTCTTCTC TTTGAATTTT	2046
TTCCAG CCT AGT CAT TGT TGG TTA CGA GAT ATG GTA ACA CAC TTA TCA	2094
Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser	
40 45 50	
GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC	2142
Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly	
55 60 65	
TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG AAA ATA GTG GAT GAC	2190
Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp	
70 75 80 85	
CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG GTA ACTTGGT ATTCATCAGA	2243
Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
90 95	
ATTATTTTTTCT TTATACTGAG CTCATGATGA GCAATTCACA ACCACTTGTA ATTCCAGCTC	2303
CAGAGGACAT TATCCCTCT TTGGATGCCA TAGGAATCTG CTCTCAAATA TG TAGATACC	2363
ACCTCTGCCA CCTCAGCACA TACATACACA TAATTAAAAA ATAGAAACAT TAAAGGAGTT	2423
CCAATCAATC CTTATTCTTT TCTGTATTCA GTATGCCAG ATGTAAATTC TAGGAATAIG	2483
TTTTAAAGGC TAATTCTTAT TTTGTAATAA GCAGCTTTAA AATTCTTAAT TGTTTTTTTCG	2543
GGTCACTTTA TTGTCCTATT GCCACGACAT TGTCCTGTCC CATTGTCTGT TATTCCTTCT	2603
GTTTTGTTTA TTGTTCCCTA GTTACTTTGA TCATGAGATT GACCTGTTAC CCGTTGTTAT	2663
TCTCTGTAGC CATTTTGAGT TGTGTCTATT AGAACAGCTG TTAAATTACT TGAATCATTG	2723
AGGACATAGT CAATAATCTA TTATGCTGAT CCAGTCAAGT CTATGAGTTA TTTGAAAAC	2783
AGAATCTTTG TTAATTATTT GTTTGCTTGT TTGTTTGT TTT ATTATTTGTC TAG AAT	2839
Asn	
GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT GAA	2887
Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu	
100 105 110	
GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC TTC	2935
Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
115 120 125	
ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA GGT	2983
Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu Gly	
130 135 140 145	
CCT GAG AAA G GTAAGGCTTT TAAGCATTTT TTGTTTAAAT GTACATAGAA	3033
Pro Glu Lys	
AGCCTGAACT TCTGTAAGCC TCTACTGCTG AATCAACTAA ATGTGTTGCT GTAGAAAGAA	3093

CGTGTGGGTT TTTCTGATAA AAACAAAAAG CAAATATCAA TGACTACCAA TGATTATTAT	3153
CTAGCTTGAG AGATATGCCC TAAGACAGCG ATTCTCGATA TTTCTAAATT AAAGAATTGT	3213
GTGATGGTGG CTCACATATT TTCTAACTGT GATATTTGCC AGGAGAGTAG AATAATGTTA	3273
TTCTTCATCC CCAGAATTCC TAAGATTTCA CGTCTCATGT CTTTTCCATA AGGTTCAAAC	3333
TCTGAGACTT GAGTTCTGAG CCTCAGCAGG TCATTCTGAA TCCCCACTCT CCCCAGAGCTG	3393
GGTCCCTATG GGGGAATAA CTTCAATTGCT TTCTTTTAAA ACATGACGAG TTACCAACAG	3453
CTCCTCGCTA TTATAACAT GTTCCTAAGC ATGTCTGTGC ATGCAATAAG CCTTCACTCT	3513
ACAAGACAGT TATGGTGTAT CGCTTGACAA AACTGAGCAG CCAAGCTGAG TATGAAATAA	3573
TAATCTAGAC TTGGGAGGCA GACCCAGCAC CTACTGTGAT ATTGCACTTC GCCTTTGGGG	3633
GACTCTATGA TTCAAAGTT CACCATGTAA CACTGACACA TTATTGCTTT CTATTAG AT	3693
	Asp
TCC AGA GTC AGT GTC AGA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC	3741
Ser Arg Val Ser Val Arg Lys Pro Phe Met Leu Pro Pro Val Ala Ala	
150 155 160 165	
AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGTAAGTACA CATATCTGAT	3794
Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
170 175	
TTACTGCATG CATGGCTCCA AGTATCCTCT ATAGGAGTGT TGCATGGACT TAAAGTTTAT	3854
AAATCACTAC TAATAATGCT GTTCTGTCAC TGTATTCTCT TGTATGGGCT TCCTGACAAT	3914
TAAATATCTG GTTTGTAGAA TCGGATCTCC TTAGAGGTTA AGATGACCAT GACAAAATTA	3974
GGCCAATCAA CTTTCTGCGA AGGTTATTTT AAATAAGGCA CGAAATTAAT TGAAGGAAAA	4034
AAAAATACAA GCAAGGCCTT ATTTTGAATC ATGGTAGGCT TAAAATAGAC TTTGTGGAGA	4094
ATGTCCCTGA TCAAAGTGGA GTTTTCAGAT TTCAAGTGCA TGTGCTAACT CTCCACAATG	4154
TCAAGGCTAT TTTCAAGTTT GTGTCTCCAT ATTTACTACT GCATGTTTGG AAATTTGCTG	4214
ATGCTGTTAG ATTACCTAAG AATGTATGTT GAAGAAGAAT GGACTTCTTT CCCTAAAATT	4274
TCTGTCCTCT TTGCCCAAGA ACCCACGTTT CTGGAAGACT ATCTTATTTT CATGTCTGTG	4334
CAATGATCAT TATAAAGATT ATTGAATATA CTGGGAATAC TCTGGTTTCT GTTTTTACAG	4394
ATTCATAATA GCTTATTCAG TCTTTAAAGA AAGTTCTCTG AAGTCCATGC TTTAGAATGT	4454
TTCTCTATCA AAACCTTGACC TGGACCTTAA ATAAAGCTAT ATTTAGTCTT TTTATCCCTG	4514
AAAAATATAT TTCACAGTGT AGACATTTGA TATACATCTA AGGGAAGGAT GCTGCCAGAA	4574
TGCTCGGGCT GGCAGTCTAC AAAGTCCACT GCTCTCAGGA TGGACTTCTG AAAGCGGAAA	4634
TTGTGAACTG CATGCATATA ACATATCAGA TCCTCGAGC	4673

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro
-20                      -15                      -10                      -5

Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val
                      1                      5                      10

Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile
                      15                      20                      25

Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp
                      30                      35                      40

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu
45                      50                      55                      60

Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile
                      65                      70                      75

Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu
                      80                      85                      90

Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg
                      95                      100                      105

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp
110                      115                      120

Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu
125                      130                      135                      140

Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg Val Ser Val Arg Lys
                      145                      150                      155

Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser
                      160                      165                      170

Ser Ser Ser Asn
175

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 26..844

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 101..844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

CTGGATCGCA GCGCTGCCTT TCCTT ATG AAG AAG ACA CAA ACT TGG ATT ATC
Met Lys Lys Thr Gln Thr Trp Ile Ile
-25                      -20

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ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT	100
Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr	
-15 -10 -5	
CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA AAA GAC ATT ACA	148
Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr	
1 5 10 15	
AAA CTG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA ACC CTC AAC TAT	196
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr	
20 25 30	
GTC GCC GGG ATG GAT GTT TTG CCT AGT CAT TGT TGG TTA CGA GAT ATG	244
Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met	
35 40 45	
GTA ACA CAC TTA TCA GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA	292
Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser	
50 55 60	
AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG	340
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly	
65 70 75 80	
AAA ATA GTG GAT GAC CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG	388
Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
85 90 95	
AAT GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT	436
Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro	
100 105 110	
GAA GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC	484
Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp	
115 120 125	
TTC ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA	532
Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu	
130 135 140	
GGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA	580
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu	
145 150 155 160	
CCC CCT GTT GCA GCC AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT	628
Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
165 170 175	
AGG AAA GCC GCA AAG TCC CCT GAA GAC CCA GGC CTA CAA TGG ACA GCA	676
Arg Lys Ala Ala Lys Ser Pro Glu Asp Pro Gly Leu Gln Trp Thr Ala	
180 185 190	
ATG GCA CTG CCG GCT CTC ATT TCG CTT GTA ATT GGC TTT GCT TTT GGA	724
Met Ala Leu Pro Ala Leu Ile Ser Leu Val Ile Gly Phe Ala Phe Gly	
195 200 205	
GCC TTA TAC TGG AAG AAG AAA CAG TCA AGT CTT ACA AGG GCA GTT GAA	772
Ala Leu Tyr Trp Lys Lys Lys Gln Ser Ser Leu Thr Arg Ala Val Glu	
210 215 220	
AAT ATA CAG ATT AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA CAG	820
Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Gln	
225 230 235 240	
AAA GAG AGA GAG TTT CAA GAG GTG TAATT	849
Lys Glu Arg Glu Phe Gln Glu Val	
245	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
-25          -20          -15          -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro
          -5          1          5

Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro
          10          15          20

Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu
          25          30          35

Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser
          40          45          50          55

Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
          60          65          70

Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val
          75          80          85

Ala Cys Met Glu Glu Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys
          90          95          100

Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe
          105          110          115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr
          120          125          130          135

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg
          140          145          150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          155          160          165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro
          170          175          180

Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile
          185          190          195

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys
          200          205          210          215

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
          220          225          230

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu
          235          240          245

Val

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152..3307, 3513..3595)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152..3307, 3513..3595)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACAAGTGAG TAGGGCGCGC CCGGGAGCTC CCAGGCTCTC CAGGAAAAAT CGCGCCCGGT	60
GCCCCGGGGA AGCCGGCGCT CCCTGGGACT TGCAGCTGGG GCGTGCAGGG CTGTGCCTGC	120
CGGGTGAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT ACAGTGTAAT	180
AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAAT GTTATTTTCA	240
AGCCGATGTG TAGGTTATGT GTGTTTCGAGA GAGAGAGAGA GAAGACAGAT TACTTTCTGC	300
TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT GGCTAAAAAG	360
CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TCGAATTCTC TTAGGTCTAA	420
AAATATACAT CTCTCTCACT TTAACCTGGT GTGCTATTGT AGATTATTGG ATTAAAGCAC	480
TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA AATAAGATGT	540
TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA AGATACCCTA	600
AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCTTA ATTGCCATTG GGAAATTGGC	660
TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT TCAAAATGGA	720
TTTTAACTAA AAGCTTTTAA AACTTTTGGT GAGCATAGCT TGAATGCGTA ATATTTAATT	780
GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTGTG GCATCAAGGC ATTAGATGTT	840
AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT CTGTTTTCAT	900
TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT	949
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn	
-20 -15 -10	
CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT	997
Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn	
-5 1 5 10	
GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC CGTGCTGTGT	1048
Val Lys Asp Val Thr Lys Leu	
15	
AAAAAAGAGC TGTGGCTCTT TTCCTGTGC TTGTTGATAA AAGATTTAGA TTTTCTTGC	1108
CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT AAAGGGTTTA	1168
TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA ACTGGCTAGT	1228

TGCACACCAC	TGCTGTGACT	GCTTCTTTTC	TGGTCTTCTC	CCCATCCTTC	ATAGGCAGTG		1288
AAGGACCTTG	GAGAGTTCGC	TGTGTGCTGA	TGGGCTTGCC	CCAGCTTGTT	CCCCATAATC		1348
TCTCCAGTGG	GTTTCCCAGC	ATGTTCTATT	CCCCTTCACA	TGTCTTCCTA	CTCTTCTTTA		1408
AAAAGCCTAA	CGAAAGGAAA	TCTGAAATGG	CTATTCTCCC	AATTCAATCA	GCAGGAAGAC		1468
CCTGTCACAT	GTCA GTGGGT	GTTTGCTCCT	TCAGGGAACA	TAGAGAGGTG	ATTCATTGCC		1528
CACATGTTGA	AGGGACTCAT	CTCCCTGGTT	TGTCACATTG	AACTCTTCCC	TCAGCGAAAAG		1588
CATTTGCATT	GCTTCCCGAA	TTCCAAGATC	ACAGGTGGAA	GCTGAAATTC	AGATCATGTT		1648
TCCAAAACTC	AGTAGGTTAT	ACCTAGCCAG	GCATAACTGA	ATTTGGAGTC	TAAAAGATCT		1708
GTATTATCAC	TTTTTTATTT	TGAAGGATGC	CTTTTGATTA	CAGAGGGAAA	TCAAGGATTA		1768
AAAATCAATA	TACATGTAAA	TATTGAAATT	CATTGGTAAC	TTTAAAAAGC	ACAACAGTTT		1828
TGTGTGCTTT	TCTCCAAAGC	ACTACAAATA	TGATTAATTG	ATGTATAAGA	ATTTTCTTAT		1888
GGAATTTTTT	TTTTTGTCTC	TGTAG	GTG	GCA AAT CTT	CCA AAA GAC TAC ATG		1940
			Val	Ala Asn Leu	Pro Lys Asp Tyr Met		
			20		25		
ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG GTATGTAAAC							1986
Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu							
30				35			
TACATTTCTG	AGTTTCATTT	TAGTAGCTCA	TAGAAGAAAT	GGGATCATTC	ATATTGAGAT		2046
AGTACACTAG	CTGCTATTTA	GGAGCTTGCT	TATTGTCAGG	ATTTGAAGAA	TTTATCTTTG		2106
GAATTTGACT	TGCAGGCTTT	TTTTTCCCCC	TCTTCCTGTT	ACAAGAGTCC	CTCCTCCTAT		2166
TACAATAGTC	CCTCCTCCTC	CTGTCACACT	AGTCCCTTCT	CTTCCTGTTA	CAATAACCCC		2226
TGTCCTCCTA	TTACAACATT	TTAAGTAATG	TAATATTAAT	TTTAAAAATC	TGGCCAGGCA		2286
CGGTGGTTCA	TGCTTGTAAT	CCCAGCACAT	TGGGAAGCTG	AGACGGGTGG	ATCATTTGAG		2346
GTCAGGAAGT	TTGAGACAGC	CTGGCCAACA	TGGTGAAACT	TCCTCTCTAC	TAAAAATAAA		2406
AAAGTAGCCA	GGCATGGTGG	CAGGCACTTG	TAATCTGAGC	TACTCGAGAG	GCTGAGGCAG		2466
GAGAATCACT	TGAGTAACTA	AAACGATAGC	TTTGAAGAGT	ACTCCGAGTT	TTATGGCACT		2526
TACTTATTAA	AATAGCTGTT	TTGTCTCTTT	TTTCATATCT	TGCAG	CCA AGT CAT		2580
					Pro Ser His		
					40		
TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT							2628
Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp							
45				50		55	
CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC							2676
Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser							
60				65		70	
ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG							2724
Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val							
75				80		85	90
AAA GAA AAC TCA TCT AAG GTAAC TTGT GTTCATTGGG ATTATTTTTC							2772
Lys Glu Asn Ser Ser Lys							
95							

ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	2832
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCAGA TGAGCAAAGA	2892
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC ATTCTTGTGT TCACTGCCCC	2952
AGATTCAACT TGTGATCCCA CTGGGATCAC TACCCTGCAT TACCAATCTG AATTACATAC	3012
GTAAAAACAG CCATCTAAAA GTGCTAGTTG TAAGAGTCTA AATACTTGAA TCTTTGAGAG	3072
ACATATTTAT AGTCCATTAT CTTACCTCA GTTAAGTCTG AAGACTATTT GAAAAATGTA	3132
ATCCTATTTT TTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC	3184
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro	
100 105	
AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT	3232
Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile	
110 115 120	
GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG	3280
Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val	
125 130 135	
GTT TCT TCA ACA TTA AGT CCT GAG AAA GGTAAGACAT GTAAGCATTT	3327
Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CCAGTTCAAA TGTAACAAC AAACCTAAAT CTTCCCTATG TAGTAAGAAT CTACCTCTGT	3387
GTAAAGCTGT AGCAAGATAC ATGCATGTAC GTCTAATAAA AAAGCAGATA TCAATAGCAC	3447
AGAAGAAACT CTATAACTCA TACAAATCAC CATATAACAC TGACACATTA TTGCTTTCTA	3507
TTTAG ATT CCA GAG TCA GTG TCA CAA AAC CAT TTA TGT TAC CCC CTG	3554
Ile Pro Glu Ser Val Ser Gln Asn His Leu Cys Tyr Pro Leu	
150 155 160	
TTG CAG CCA GCT CCC TTA GGA ATG ACA GCA GTA GCA GTA ATAGTAAGTA	3603
Leu Gln Pro Ala Pro Leu Gly Met Thr Ala Val Ala Val	
165 170 175	
CATATATCTG ATTTAATGCA TGCATGGCTC CAATTAGCAC CTATAGGAGT ATTGCATGGG	3663
CTTTCAAGGA AACTTCTACA TTTATTATTA TTGATACTGT TCTGTACTG TTATTCCTTT	3723
TATGGTCTTC TTGAGACTTA AGTTTGTAGA ATTAAATTTT CCTAGAGCTG GAGATAATGT	3783
TTAGAGAATT AGGCCAATAA ATTT	3807

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro
-20 -15 -10 -5
Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val

	1		5		10										
Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	Tyr	Met	Ile
	15						20					25			
Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp
	30					35					40				
Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu
	45				50				55					60	
Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile
				65					70					75	
Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu
			80					85					90		
Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg
		95				100						105			
Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp
	110					115					120				
Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val
	125				130					135					140
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Ile	Pro	Glu	Ser	Val	Ser	Gln	Asn
			145					150						155	
His	Leu	Cys	Tyr	Pro	Leu	Leu	Gln	Pro	Ala	Pro	Leu	Gly	Met	Thr	Ala
		160					165						170		
Val	Ala	Val													
		175													

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 17..640

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 92..640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAGCTTGCCT TTCCTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC	49
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys	
-25 -20 -15	
ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG	97
Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly	
-10 -5 1	
ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG	145
Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu	

5	10	15	
GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC			193
Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro			
20	25	30	
GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA			241
Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val			
35	40	45	50
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT			289
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile			
55	60	65	
TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA			337
Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile			
70	75	80	
GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA			385
Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu			
85	90	95	
AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA			433
Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu			
100	105	110	
TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA			481
Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val			
115	120	125	130
GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT			529
Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro			
135	140	145	
GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT			577
Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro			
150	155	160	
GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGT AAG			625
Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys			
165	170	175	
TAC ATA TAT CTG ATT TAATGCATGC ATGGCTCCAA TTAGCACCTA TAGGAGTATT			680
Tyr Ile Tyr Leu Ile			
180			
GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG ATACTGTTCT GTTACTGTTA			740
TTCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT AAATTTCCCT AGAGCTGGAG			800
ATAATGTTTA GAGAATTAGG			820

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25 -20 -15 -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg

-5	1	5		
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro	10	15	20	
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	25	30	35	
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser	40	45	50	55
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser	60	65	70	
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val	75	80	85	
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys	90	95	100	
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe	105	110	115	
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr	120	125	130	135
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg	140	145	150	
Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser	155	160	165	
Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys Tyr Ile Tyr Leu Ile	170	175	180	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAGCTCCGAG CCCTCTCTGG CGCGCGAGGT ATTCGTCCTG TNCCCGGGGG TGCCAGGTGA	60
GCCCCAGCGG ATCCGGGAGG GTAAGCTGGG ACTCCTCGCG AGCAGTAGCT GCAGGGTACC	120
AAGCTTCGCC CTCTGCGTCC CCGCGCCTTC GCGGTCTCCC GCCAGTGCAG GTCCGGGGCC	180
CCCAGGCGAG CGGACAAGGT TGGCCTAATC TGCCAACTT CTGGGGCATT TACCGTGCTC	240

TGGCCGCCCT CCCGATTCTT CCCTCCGCGC CTTTGCCTGC TTCTCGCCTA CCCCGGGCTC	300
CGGAAGGGAA GGAGGCGTGT CCGGAGCAGG CGGGCGGGAA CTGTATAAAA GCGCCGGCGG	360
CTCAGCAGCC GGCTTCGCTC GCCGCCTCGC GCCGAGACTA GAAGCGCTGC GGGGAAGCAGG	420
GACAGTGGAG AGGGCGCTGC GCTCGGGCTA CCCAATGCGT GGACTATCTG CCGCCGCTGT	480
TCGTGCAATA TGCTGGAGCT CCAGAACAGC TAAACGGAGT CGCCACACCA CTGTTTGTGC	540
TGGATCGCAC CGCTGCCTTT CTT ATG AAG AAG ACA CAA GTGAGTAGGG	589
Met Lys Lys Thr Gln	
-25	
CGCGCCCGGG AGCTCCCAGG CTCTCCAGGA AAAATCGCGC CCGGTGCCCC GGGGAAGCCG	649
GCGCTCCCTG GGACTTGCGAG CTGGGGCGTG CAGGGCTGTG CTGCGCGGT GAGACAAGAG	709
GATGCGGGGG AGGCCGGCGT GGTGTGTGAT CCCGAGCCGA GCCGNNTGAG CCAGGGAGAA	769
AAGGAGTGGG AGTACTGAGA GGGAGCCAGT GTCAAGTTTG GAGCCTCAGC AGTTAAGTTT	829
TGAGCTGTCA GTCGGAAACC GTAATTCCTG TCTGGTGGA AGATTGGCTT TTNGNCCACG	889
GAATGTAAGT TATCACAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT	949
ACAGTGTAAT AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT	1009
GTTATTTTCA AGCCGATGTG TAGGTTATGT GTGTTGAGA GAGAGAGAGA GAAGACAGAT	1069
TACTTTCTGC TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT	1129
GGCTAAAAAG CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATT'CAG TGGAAATTCTC	1189
TTAGGTCTAA AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG	1249
ATTAAAGCAC TGCTCAGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA	1309
AATAAGATGT TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA	1369
AGATACCCTA AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCTTA ATTGCCATTG	1429
GGAAATTGGC TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT	1489
TCAAAATGGA TTTTAAGTAA AAGCTTTTAA AAAGTTTGGT GAGCATAGCT TGAATGCGTA	1549
ATATTTAATT GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTGT GCATCAAGGC	1609
ATTAGATGTT AAAAGTTTGA ATGATTACAG ATCTTAAGT ATGATCACCA AGCAATTTT	1669
CTGTTTTTCA TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC	1719
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu	
-20 -15 -10	
CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG	1767
Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val	
-5 1 5	
ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC	1817
Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
10 15	
CGTGCTGTGT AAAAAAGAGC TGTGGCTCTT TTTCCTGTGC TTGTTGATAA AAGATTTAGA	1877
TTTTTCTTGC CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT	1937
AAAGGGTTTA TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA	1997

ACTGGCTAGT TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC	2057
ATAGGCAGTG AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT	2117
CCCCATAATC TCTCCAGTGG GTTTCCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCTTA	2177
CTCTTCTTTA AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA	2237
GCAGGAAGAC CCTGTACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG	2297
ATTCATTGCC CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC	2357
TCAGCGAAAG CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC	2417
AGATCATGTT TCCAAACTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC	2477
TAAAAGATCT GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTGTGATTA CAGAGGGAAA	2537
TCAAGGATTA AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC	2597
ACAACAGTTT TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA	2657
ATTTTCTTAT GGAATTTTTT TTTTGTCTC TG TAG GTG GCA AAT CTT CCA AAA	2710
Val Ala Asn Leu Pro Lys	
20	
GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG	2755
Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	
GATGTAAAC TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC	2815
ATATTGAGAT AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA	2875
TTTATCTTTG GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC	2935
CTCCTCCTAT TACAATAGTC CCTCCTCCTC CTGTACACT AGTCCCTTCT CTTCTGTTA	2995
CAATAACCCC TGTCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC	3055
TGGCCAGGCA CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG	3115
ATCATTTGAG GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC	3175
TAAAAATAAA AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG	3235
GCTGAGGCAG GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT	3295
TTATGGCACT TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA	3353
Pro	
40	
AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG	3401
Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu	
45 50 55	
ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT	3449
Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn	
60 65 70	
TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG	3497
Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu	
75 80 85	
TGC GTG AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	3551
Cys Val Lys Glu Asn Ser Ser Lys	
90 95	

ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	3611
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTCAGA TGAGCAAAGA	3671
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC TATTCTTGTG TTCACTGCCC	3731
CAGATTCAAC TTGTGATCCC ACTGGGATCA CTACCCTGCA TTACCAATCT GAATTACATA	3791
CGTTAAACA GCCATCTAAA AGTGCTAGTT GTAAGAGTCT AAATACTTGA ATCTTTGAGA	3851
GACATATTTA TAGTCCATTA TCTTCACCTC AGTTAAGTCT GAAGACTATT TGAAAAATGT	3911
AATCCTATTT TTTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA	3961
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu	
100 105	
CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC	4009
Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser	
110 115 120	
ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT	4057
Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys	
125 130 135	
GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA G GTAAGACATG TAAGCATTTC	4108
Val Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CAGTTCAAAT GTAAACAACA AACTTAAATC TTCCCTATGT AGTAAGAATC TACCTCTGTG	4168
TTAAGCTGTA GCAAGATACA TGCATGTACG TCTAAAAAAA AGCAGATATC AATAGCACAG	4228
AAGAACTAA TGATTGTAGA TTTGTGGGCT CTATAACTCA TACAAATCAC CATATAACAC	4288
TGACACATTA TTGCTTTCTA TTTAG AT TCC AGA GTC AGT GTC ACA AAA CCA	4339
Asp Ser Arg Val Ser Val Thr Lys Pro	
150 155	
TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT	4387
Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser	
160 165 170	
AGC AGT AAT A GTAAGTACAT ATATCTGATT TAATGCATGC ATGGCTCCAA	4437
Ser Ser Asn	
175	
TTAGCACCTA TAGGAGTATT GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG	4497
ATACTGTTCT GTTACTGTTA TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT	4557
AAATTTCCCT AGAGCTGGAG ATAATGTTTA GAGAATTAGG CCAATAAATT TTCTGCTGAG	4617
GTTATTTTAA ATAAGACATA AAATTAATTT TAGAAATATG ATTTATGCCT TTTGTTGAAT	4677
CATTAACATA TATACAGAAA CAGTTAAAC AACCACAGCA TAAGAGAAAA ACTTCTAGAA	4737
TGGATATGCT GTATTCATCA GTGTGTTCTT TAAATTATAG GG AAG GCC AAA AAT	4791
Arg Lys Ala Lys Asn	
180	
CCC CCT GGA GAC TCC AGC CTA CAC TGG CCA GCC ATG GCA TTG CCA GCA	4839
Pro Pro Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala	
185 190 195	
TTG TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG	4887
Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys	
200 205 210	

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu
-25					-20					-15					-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg
				-5					1				5		
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro
		10					15					20			
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu
	25					30					35				
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser
40					45					50					55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
60 65 70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
75 80 85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
90 95 100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
105 110 115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
120 125 130 135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
140 145 150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
155 160 165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
170 175 180

Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala Leu Phe
185 190 195

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
200 205 210 215

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser

85								90				95				
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	
			100							105				110		
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	
			115				120							125		
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	
			130				135							140		
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	
			145				150							155	160	
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	
			165							170				175		
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	
			180							185				190		
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	
			195				200							205		
Gly	Asp	Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	
			210				215							220		
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	
			225				230							235	240	
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	
			245							250				255		
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	
			260							265				270		
Val																

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu
1				5					10					15	
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg
			20					25					30		
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro
		35					40					45			
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu
	50					55					60				
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser
65					70					75					80
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser
				85					90					95	

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Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
      100                      105                      110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
      115                      120                      125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
      130                      135                      140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Ala Val Ala Ser Glu Thr
      145                      150                      155                      160

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
      165                      170                      175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
      180                      185                      190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Thr
      195                      200                      205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Phe Phe
      210                      215                      220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
      225                      230                      235                      240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
      245                      250                      255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
      260                      265                      270

Val

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(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1      5      10      15

Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Gly Ile Cys Gly Lys Arg
      20      25      30

Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
      35      40      45

Lys Asp Tyr Lys Ile Ala Leu Lys Tyr Val Pro Gly Met Asp Val Leu
      50      55      60

Pro Ser His Cys Trp Ile Ser Val Met Val Glu Gln Leu Ser Val Ser
      65      70      75      80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
      85      90      95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val
      100      105      110

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Glu Cys Thr Glu Gly Tyr Ser Phe Glu Asn Val Lys Lys Ala Pro Lys
115 120 125

Ser Pro Glu Leu Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Leu Glu Thr Val Ala Ser Lys
145 150 155 160

Ser Ser Glu Cys Val Val Ser Ser Thr Leu Ser Pro Asp Lys Asp Ser
165 170 175

Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser
180 185 190

Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser
195 200 205

Ile Gly Asp Ser Asn Leu Gln Trp Ala Ala Met Ala Leu Pro Ala Phe
210 215 220

Phe Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys
225 230 235 240

Lys Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu
245 250 255

Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln
260 265 270

Glu Val

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Thr Gln Thr Trp Ile Val Thr Cys Ile Tyr Leu Gln Leu Leu
1 5 10 15

Phe Asn Pro Leu Val Lys Thr Lys Gly Leu Cys Arg Asn Arg Val Thr
20 25 30

Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp
35 40 45

Tyr Lys Ile Ala Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser
50 55 60

His Cys Trp Ile Ser Val Met Val Glu Gln Leu Ser Val Ser Leu Thr
65 70 75 80

Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr
85 90 95

Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val Glu Cys
100 105 110

Val Glu Gly His Ser Ser Glu Asn Val Lys Lys Ser Ser Lys Ser Pro
115 120 125

Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg
130 135 140

Ser Ile Asp Ala Phe Lys Asp Leu Glu Met Val Ala Ser Lys Thr Ser
145 155 160

Glu Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val
165 170 175

Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu
180 185 190

Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Thr Asn Pro Ile Glu Asp
195 200 205

Ser Ser Ile Gln Trp Ala Val Met Ala Leu Pro Ala Cys Phe Ser Leu
210 215 220

Val Ile Gly Phe Ala Phe Gly Ala Phe Tyr Trp Lys Lys Lys Gln Pro
225 230 235 240

Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn
245 250 255

Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu Val
260 265 270

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val His Thr Gln Gly Ile Cys Ser Asn Arg
20 25 30

Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Cys Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val
100 105 110

Glu Cys Met Glu His Ser Ser Glu Asn Val Lys Lys Ser Ser Lys Ser
115 120 125

Pro Glu Pro Arg Gln Phe Thr Pro Glu Lys Phe Phe Gly Ile Phe Asn
130 135 140

Lys Ser Ile Asp Ala Phe Lys Asp Leu Glu Ile Val Ala Ser Lys Met
 145 150 155 160
 Ser Glu Cys Val Ile Ser Ser Thr Ser Ser Pro Glu Lys Asp Ser Arg
 165 170 175
 Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
 180 185 190
 Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser Ile
 195 200 205
 Glu Asp Ser Ser Leu Gln Trp Ala Ala Val Ala Leu Pro Ala Phe Phe
 210 215 220
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Phe Tyr Trp Lys Lys Lys
 225 230 235 240
 Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Arg Gln Ile Asn Glu Glu
 245 250 255
 Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
 260 265 270
 Val

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
 1 5 10 15
 Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro
 20 25 30
 Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro
 35 40 45
 Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu
 50 55 60
 Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser
 65 70 75 80
 Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
 85 90 95
 Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val
 100 105 110
 Ala Cys Met Glu Glu Asn Ala Pro Leu Asn Val Lys Glu Ser Leu Lys
 115 120 125
 Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe
 130 135 140
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr
 145 150 155 160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro
195 200 205

Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile
210 215 220

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys
225 230 235 240

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu
260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Glu Ile Cys Gly Asn Pro
20 25 30

Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Leu Arg Asp Met Val Ile Gln Leu Ser Leu Ser
65 70 75 80

Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val
100 105 110

Leu Cys Met Glu Glu Asn Ala Pro Lys Asn Ile Lys Glu Ser Pro Lys
115 120 125

Arg Pro Glu Thr Arg Ser Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr
145 150 155 160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg
165 170 175

Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser
			180					185					190		
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ala	Lys	Ala	Pro
		195					200				205				
Glu	Asp	Ser	Gly	Leu	Gln	Trp	Thr	Ala	Met	Ala	Leu	Pro	Ala	Leu	Ile
	210					215					220				
Ser	Leu	Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Lys
225				230						235					240
Gln	Ser	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu
				245					250					255	
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Gln	Lys	Glu	Arg	Glu	Phe	Gln	Glu
			260					265					270		

Val

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr	Trp	Ile	Ile	Thr	Cys	Phe	Cys	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Pro
1				5					10					15	
Leu	Val	Lys	Ala	Gln	Ser	Ser	Cys	Gly	Asn	Pro	Val	Thr	Asp	Asp	Val
			20					25					30		
Asn	Asp	Ile	Ala	Lys	Leu	Val	Gly	Asn	Leu	Pro	Asn	Asp	Tyr	Leu	Ile
		35					40					45			
Thr	Leu	Lys	Tyr	Val	Pro	Lys	Met	Asp	Ser	Leu	Pro	Asn	His	Cys	Trp
	50					55					60				
Leu	His	Leu	Met	Val	Pro	Glu	Phe	Ser	Arg	Ser	Leu	His	Asn	Leu	Leu
65					70					75					80
Gln	Lys	Phe	Ser	Asp	Ile	Ser	Asp	Met	Ser	Asp	Val	Leu	Ser	Asn	Tyr
				85					90					95	
Ser	Ile	Ile	Asn	Asn	Leu	Thr	Arg	Ile	Ile	Asn	Asp	Leu	Met	Ala	Cys
			100					105					110		
Leu	Ala	Phe	Asp	Lys	Asn	Lys	Asp	Phe	Ile	Lys	Glu	Asn	Gly	Leu	His
		115					120					125			
Tyr	Glu	Glu	Asp	Arg	Phe	Ile	Pro	Glu	Asn	Phe	Phe	Arg	Leu	Phe	Asn
	130					135					140				
Ser	Thr	Ile	Glu	Val	Tyr	Lys	Glu	Phe	Ala	Asp	Ser	Leu	Asp	Lys	Asn
145					150					155					160
Asp	Cys	Ile	Met	Pro	Ser	Thr	Val	Glu	Thr	Pro	Glu	Asn	Asp	Ser	Arg
				165					170					175	
Val	Ala	Val	Thr	Lys	Thr	Ile	Ser	Phe	Pro	Pro	Val	Ala	Ala	Ser	Ser
			180					185					190		

Leu Arg Asn Asp Ser Ile Gly Ser Asn Thr Ser Ser Asn Ser Asn Lys
 195 200 205

Glu Ala Leu Gly Phe Ile Ser Ser Ser Ser Leu Gln Gly Ile Ser Ile
 210 215 220

Ala Leu Thr Ser Leu Leu Ser Leu Leu Ile Gly Phe Ile Leu Gly Ala
 225 230 235 240

Ile Tyr Trp Lys Lys Thr His Pro Lys Ser Arg Pro Glu Ser Asn Glu
 245 250 255

Thr Ile Gln Cys His Gly Cys Gln Glu Glu Asn Glu Ile Ser Met Leu
 260 265 270

Gln Gln Lys Glu Lys Glu His Leu Gln Val
 275 280

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
 1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Gly Ile Cys Arg Asn Arg Val
 20 25 30

Thr Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp
 35 40 45

Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser
 50 55 60

His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser Leu Thr
 65 70 75 80

Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr
 85 90 95

Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val Glu Cys
 100 105 110

Glu Glu Asn Ser Ser Lys Asn Val Lys Lys Ser Lys Ser Pro Glu Pro
 115 120 125

Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile
 130 135 140

Asp Ala Phe Lys Asp Phe Met Val Ala Ser Lys Thr Ser Asp Cys Val
 145 150 155 160

Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
 165 170 175

Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp
 180 185 190

Ser Ser Ser Ser Asn Arg Lys Ala Asn Glu Asp Ser Ser Leu Gln Trp
 195 200 205
 Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Val Ile Gly Phe Ala
 210 215 220
 Phe Gly Ala Leu Tyr Trp Lys Lys Lys Gln Pro Ser Leu Thr Arg Ala
 225 230 235 240
 Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu
 245 250 255
 Gln Glu Lys Glu Arg Glu Phe Gln Glu Val
 260 265

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..210, 223..258)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAA TTC TTC CGT ATC TTC AAC CGT TCC ATC GAC GCT TTC AAA GAC TTC	48
Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
GTT GTT GCT TCC GAA ACC TCC GAC TGC GTT GTT TCC TCC ACC CTG TCT	96
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
CCG GAA AAA GAC TCC CGT GTT TCG GTT ACC AAA CCG TTC ATG CTG CCG	144
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
CCG GTT GCT GCT TCC TCC CTG CGT AAC GAC TCC TCC TCC TCC AAC TCC	192
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Asn Ser	
50 55 60	
AAA TAC ATC TAC CTG ATC TAATAGGATC CG GTT ACC AAA CCG TTC ATG	240
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met	
65 70 75	
CTG CCG CCG GTT GCT GCT TAATAGGATC C	269
Leu Pro Pro Val Ala Ala	
80	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe

1	5	10	15
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser			
20	25	30	
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro			
35	40	45	
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser			
50	55	60	
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met Leu Pro Pro Val			
65	70	75	80

Ala Ala

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 184..1002

- (ix) FEATURE:
- (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 259..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGCCTCGCG CCGAGACTAG AAGCGCTGCG GGAAGCAGGG ACAGTGGAGA GGGCGCTGCG	60
CTCGGGCTAC CCAATGCGTG GACTATCTGC CGCCGCTGTT CGTGCAATAT GCTGGAGCTC	120
CAGAACAGCT AAACGGAGTC GCCACACCAC TGTTTGTGCT GGATCGCAGC GCTGCCTTTC	180
CTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG	228
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln	
-25 -20 -15	
CTG CTC CTA ITT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT	276
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn	
-10 -5 1 5	
CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA AAT CTT	324
Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu	
10 15 20	
CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT	372
Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val	
25 30 35	
TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC	420
Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp	
40 45 50	
AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG	468
Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu	
55 60 65 70	
AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT	516

Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu	75	80	85	
GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA AAA AAA TCA TTC				564
Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe	90	95	100	
AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT				612
Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile	105	110	115	
TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA				660
Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu	120	125	130	
ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC				708
Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser	135	140	145	150
AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC				756
Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser	155	160	165	
TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC				804
Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro	170	175	180	
CCT GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG				852
Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu	185	190	195	
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG				900
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys	200	205	210	
AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA				948
Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu	215	220	225	230
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA				996
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln	235	240	245	
GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA				1052
Glu Val				
GTTCATGTTT GCTTCATAAA TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA				1112
CAGACCACAT CTTTATCTGT TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG				1172
GAACAGAATG TTTTACTGTG AAAGTGGCAC TGAATTAATC ATCTATAAAG AAGAACTTGC				1232
ATGGAGCAGG ACTCTATTTT AAGGACTGCG GGAAGTGGGT CTCATTTAGA ACTTGCAGCT				1292
GATGTTGGAA GAGAAAGCAC GTGTCTCAGA CTGCATGTAC CATTTCATG GCTCCAGAAA				1352
TGTCTAAATG CTGAAAAAAC ACCTAGCTTT ATTCTTCAGA TACAACTGC AG				1404

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25          -20          -15          -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
          -5          1          5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
          10          15          20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
          25          30          35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
          40          45          50          55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
          60          65          70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
          75          80          85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
          90          95          100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
          105          110          115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
          120          125          130          135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
          140          145          150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          155          160          165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
          170          175          180

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe
          185          190          195

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
          200          205          210          215

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
          220          225          230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
          235          240          245

Val

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(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 151..885

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 226..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCAGGGACA GTGGAGAGGG CGCTGCGCTC GGGCTACCCA ATGCGTGGAC TATCTGCCGC	60
CGCTGTTTCGT GCAATATGCT GGAGCTCCAG AACAGCTAAA CGGAGTCGCC ACACCACTGT	120
TTGTGCTGGA TCGCAGCGCT GCCTTTCCTT ATG AAG AAG ACA CAA ACT TGG ATT	174
Met Lys Lys Thr Gln Thr Trp Ile	
-25 -20	
CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA	222
Leu Thr Cys Ile Tyr Leu Gln Leu Leu Phe Asn Pro Leu Val Lys	
-15 -10 -5	
ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC	270
Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val	
1 5 10 15	
ACT AAA TTG GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA	318
Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys	
20 25 30	
TAT GTC CCC GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG	366
Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu	
35 40 45	
ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT	414
Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe	
50 55 60	
TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT	462
Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu	
65 70 75	
GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	510
Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	
80 85 90 95	
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT	558
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr	
100 105 110	
CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG	606
Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys	
115 120 125	
GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA	654
Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr	
130 135 140	
TTA AGT CCT GAG AAA GGG AAG GCC AAA AAT CCC CCT GGA GAC TCC AGC	702
Leu Ser Pro Glu Lys Gly Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser	
145 150 155	
CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT CTT ATA ATT	750
Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Ile Ile	
160 165 170 175	

GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA CAG CCA AGT CTT	798
Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg Gln Pro Ser Leu	
180 185 190	
ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA	846
Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile	
195 200 205	
AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA GAA GTG TAATTGTGGC	895
Ser Met Lys Gln Glu Lys Glu Arg Glu Phe Gln Glu Val	
210 215 220	
TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA GTTCATGTTT GCTTCATAAA	955
TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA CAGACCACAT CTTTATCTGT	1015
TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG GAACAGAATG TTTTACTGTG	1075
AAACTGGCAC TGA	1088

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu	
-25 -20 -15 -10	
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg	
-5 1 5	
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro	
10 15 20	
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser	
40 45 50 55	
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser	
60 65 70	
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val	
75 80 85	
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys	
90 95 100	
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe	
105 110 115	
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr	
120 125 130 135	
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala	
140 145 150	
Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu	
155 160 165	

Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr
 170 175 180
 Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln
 185 190 195
 Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
 200 205 210 215
 Glu Phe Gln Glu Val
 220

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr
 1 5 10 15
 Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr
 20 25 30
 Val Ala Gly Met Asp Val Leu Pro Ser His Xaa Trp Leu Arg Asp
 35 40 45

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ile Thr Thr Leu Asn Tyr Val Ala Gly Met
 1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Xaa Xaa Leu Gly Pro
 1 5 10 15
 Glu Lys Asp Ser Arg Val Ser Val Xaa Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Ala Pro Lys Asn Val Glu Ser Leu Lys Lys Pro Thr Arg
1 5 10 15

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asp Arg Ser Ile Asp
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Glu Ser Leu Lys Lys Pro Glu Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Ser Val Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile	Val	Asp	Asp	Leu	Val	Ala	Ala	Met	Glu	Glu	Asn	Ala	Pro	Lys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	Xaa	Arg
1				5					10			

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val
1				5					10					15	

Ala	Gly	Asp	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg
				20				25				

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp
1				5					10					15	

Cys	Val	Leu	Ser	Xaa	Xaa	Leu	Gly
						20	

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe
1 5 10 15
Phe Ser Ile Phe Xaa Arg
20

(2) INFORMATION FOR SEO ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe
1 5 10 15
Phe Ser Ile Phe Asp Arg
20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn Ala Pro Lys Asn Val Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Arg Val Ser Val Xaa Lys Pro Phe Met Leu Pro Pro Val Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala
20 25 30

Ser Asp Thr Ser Asp
35

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu
1 5 10 15

Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile
20 25 30

Asp Lys Leu Gly Lys Ile Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Pro Val Ala Ala
1

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTGAGAAAG ATTCCAGAGTC

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGCAGTTTG TATCTGAAG

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CATATAAAGT CATGGGTAG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACTTGTGTCT TCTTCATAAG GAAAGGC

27

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTACGAAAG TAACAGTGTT G

21

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACTGCTCCTA TTTAATCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGACTCT GGAATCTTTC TCA

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGACCCGGA TCCCC

15

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCGAGGGGAT CCGGG

15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTTCTTCAT GGCGGCGGCA AGCTT

25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Ser	Arg	Val	Ser	Val	Xaa	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5					10				15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5					10				15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGGGAATTC GGTAC 55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT 49

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAGGA 9

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCTCCTGC A 11

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGGAAGGT ATCTGCA 17

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATACCTTCC A

11

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTCCTTATG

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCCGCCGCCA TG

12

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TCTTCTTCAT GCGGCGGCA AGCTT

25